

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Huse, William D.
- (ii) TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human Antibodies, Nucleic Acids Encoding Same and Methods of Use
- (iii) NUMBER OF SEQUENCES: 24
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Campbell & Flores LLP
 - (B) STREET: 4370 La Jolla Village Drive, Suite 700
 - (C) CITY: San Diego
 - (D) STATE: California
 - (E) COUNTRY: United States (F) ZIP: 92122
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/790,540
 - (B) FILING DATE: 30-JAN-1997
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Campbell, Cathryn A.
 - (B) REGISTRATION NUMBER: 31,815
 - (C) REFERENCE/DOCKET NUMBER: P-IX 2405
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (619) 535-9001
 - (B) TELEFAX: (619) 535-8949
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 351 base pairs

 - (B) TYPE: nucleic acid (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..351
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
- CAG GTG CAG CTG GTG GAG TCT GGG GGA GGC GTT GTG CAG CCT GGA AGG 48 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
- 96 TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC ACC TTC AGT AGC TAT Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr 20
- GAC ATG TCT TGG GTT CGC CAG GCT CCG GGC AAG GGT CTG GAG TGG GTC 144 Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val



GCA Ala	AAA Lys 50	GTT Val	AGT Ser	AGT Ser	GGT Gly	GGT Gly 55	GGT Gly	AGC Ser	ACC Thr	TAC Tyr	TAT Tyr 60	TTA Leu	GAC Asp	ACT Thr	GTG Val	192
				ACC Thr												240
				TCT Ser 85												288
GCA Ala	AGA Arg	CAT His	AAC Asn 100	TAC Tyr	GGC Gly	AGT Ser	TTT Phe	GCT Ala 105	TAC Tyr	TGG Trp	GGC Gly	CAA Gln	GGG Gly 110	ACT Thr	ACA Thr	336
			TCT Ser													351

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 117 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45

Ala Lys Val Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Leu Asp Thr Val

Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser 115

- (2) INFORMATION FOR SEQ ID NO:3:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 321 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS



(B) LOCATION: 1..321

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:															
GAG Glu 1	ATT Ile	GTG Val	CTA Leu	ACT Thr 5	CAG Gln	TCT Ser	CCA Pro	GCC Ala	ACC Thr 10	CTG Leu	TCT Ser	CTC Leu	AGC Ser	CCA Pro 15	GGA Gly	48
GAA Glu	AGG Arg	GCG Ala	ACT Thr 20	CTT Leu	TCC Ser	TGC Cys	CAG Gln	GCC Ala 25	AGC Ser	CAA Gln	AGT Ser	ATT Ile	AGC Ser 30	AAC Asn	CAC His	96
CTA Leu	CAC His	TGG Trp 35	TAT Tyr	CAA Gln	CAA Gln	AGG Arg	CCT Pro 40	GGT Gly	CAA Gln	GCC Ala	CCA Pro	AGG Arg 45	CTT Leu	CTC Leu	ATC Ile	144
MKK Xaa	TAT Tyr 50	CGT Arg	TCC Ser	CAG Gln	TCC Ser	ATC Ile 55	TCT Ser	GGG Gly	ATC Ile	CCC Pro	GCC Ala 60	AGG Arg	TTC Phe	AGT Ser	GGC Gly	192
AGT Ser 65	GGA Gly	TCA Ser	GGG Gly	ACA Thr	GAT Asp 70	TTC Phe	ACC Thr	CTC Leu	ACT Thr	ATC Ile 75	TCC Ser	AGT Ser	CTG Leu	GAG Glu	CCT Pro 80	240
GAA Glu	GAT Asp	TTT Phe	GCA Ala	GTC Val 85	TAT Tyr	TAC Tyr	TGT Cys	CAA Gln	CAG Gln 90	AGT Ser	GGC Gly	AGC Ser	TGG Trp	CCT Pro 95	CAC His	288
					ACC Thr											321



(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 107 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Gln Ala Ser Gln Ser Ile Ser Asn His 20 25 30

Leu His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile 35 40

Xaa Tyr Arg Ser Gln Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro 65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Gly Ser Trp Pro His 85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 351 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

					GTG Val			48
					GCT Ala			96
					AGG Arg			144
					TAT Tyr 60			192
					AAG Lys			240
					GCC Ala			288
					GGC Gly			336

351

(2) INFORMATION FOR SEQ ID NO:6:

GTC ACT GTC TCT GCA Val Thr Val Ser Ala

115

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 117 amino acids
 - (B) TYPE: amino acid(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Arg

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Ser Ser Tyr 20



Asp Met Ser Trp Val Arg Gln Ile Pro Glu Lys Arg Leu Glu Trp Val 40 Ala Lys Val Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Leu Asp Thr Val 55 60 Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu Gln Met Ser Ser Leu Asn Ser Glu Asp Thr Ala Met Tyr Tyr Cys
85 90 95 Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala 115

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 321 base pairs (B) TYPE: nucleic acid

 - (C) STRANDEDNESS: single (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

					CTG Leu			48
					CAA Gln			96
					TCT Ser			144
					CCC Pro			192
					ATC Ile 75			240
					AGT Ser			288
TTC Phe								321

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 107 amino acids



(B) TYPE: amino acid(D) TOPOLOGY: linear

	()	Li) N	OLE	CULE	TYPE	E: pı	cote	in									
	()	(i) S	SEQUE	ENCE	DESC	CRIPT	LION	: SE) ID	NO:	3:						
Asp 1	Ile	Val	Leu	Thr 5	Gln	Ser	Pro	Ala	Thr 10	Leu	Ser	Val	Thr	Pro 15	Gly		
Asp	Ser	Val	Ser 20	Leu	Ser	Сув	Gln	Ala 25	Ser	Gln	Ser	Ile	Ser 30	Asn	His		
Leu	His	Trp 35	Tyr	Gln	Gln	Lys	Ser 40	His	Glu	Ser	Pro	Arg 45	Leu	Leu	Ile		
Lys	Tyr 50	Arg	Ser	Gln	Ser	Ile 55	Ser	Gly	Ile	Pro	Ser 60	Arg	Phe	Ser	Gly		
Ser 65	Gly	Ser	Gly	Thr	Asp 70	Phe	Ala	Leu	Ser	Ile 75	Asn	Ser	Val	Glu	Thr 80		
Glu	Asp	Phe	Gly	Met 85	Tyr	Phe	Cys	Gln	Gln 90	Ser	Gly	Ser	Trp	Pro 95	His		
Thr	Phe	Gly	Gly 100	Gly	Thr	Lys	Leu	Glu 105	Ile	Lys							
(2)	TNEC	יבאסר		AOA	SEQ	י מד	10 · 9										
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	(xi)	SEÇ	QUENC	CE DI	ESCRI	PTIC	ON: S	SEQ I	D NO	0:9:							
CAG	GTGC#	AGC 7	rggto	GAG	C TO	GGGG	BAGG	C GT	rgtgo	CAGC	CTG	BAAG	GTC (CCTG	AGACT	С	60
TCCT	rgtgo	CAG (CCTC	rgga:	T C	ACC											84
(2)	INFO	ORMAT	rion	FOR	SEQ	ID 1	10:10	0:									
	(i)	SEC	UENC	CE CI	IARAC	TER	STI	CS:									
	, ,	(2	A) LI	ENGTI	I: 84	l bas	se pa	airs									
					nuc] EDNE												
		(I) TO	POLO	GY:	line	ear										
	(xi)	SEÇ	QUENC	CE DI	ESCRI	PTIC	ON: S	SEQ I	D NO	0:10	:						
AACT	TTTT	GCG A	ACCC	CTC	CA GA	ACCCI	TGC	c cgo	BAGC	CTGG	CGA	ACCC	AAG 2	ACAT	GTCAT.	A	60
GCT	ACTGA	AAG (TGA	ATCC	AG AG	GC											84
(2)	INFO	ORMAT	MOIT	FOR	SEQ	ID 1	10:13	L:									
	(i)		-		IARAC												
		(<i>I</i>	1) LE 3) TY	INGTI (PE :	I: 87 nucl	/ bas Leic	se pa acio	airs									
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		(I)) TC	POLC	GY:	line	ear										

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:	
TGGGTCGCAA AAGTTAGTAG TGGTGGTGGT AGCACCTACT ATTTAGACAC TGTGCAGGGC	60
CGATTCACCA TCTCCAGAGA CAATAGT	87
(2) INFORMATION FOR SEQ ID NO:12:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 81 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:	
TGCACAGTAA TACACGGCTG TGTCCTCGGC TCTCAGAGAG TTCATTTGCA GGTATAGGGT	60
GTTCTTACTA TTGTCTCTGG A	81
(2) INFORMATION FOR SEQ ID NO:13:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 75 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:	
GTGTATTACT GTGCAAGACA TAACTACGGC AGTTTTGCTT ACTGGGGCCA AGGGACTACA	60
GTGACTGTTT CTAGT	75
(2) INFORMATION FOR SEQ ID NO:14:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 87 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:	
GAGATTGTGC TAACTCAGTC TCCAGCCACC CTGTCTCTCA GCCCAGGAGA AAGGGCGACT	60
CTTTCCTGCC AGGCCAGCCA AAGTATT	87
(2) INFORMATION FOR SEQ ID NO:15:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 75 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:	
TTAGATGAGA AGCCTTGGGG CTTGACCAGG CCTTTGTTGA TACCAGTGTA GGTGGTTGCT	60
AATACTTTGG CTGGC	75
(2) INFORMATION FOR SEQ ID NO:16:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 84 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:	
CCAAGGCTTC TCATCTAATA TCGTTCCCAG TCCATCTCTG GGATCCCCGC CAGGTTCAGT	60
GGCAGTGGAT CAGGGACAGA TTTC	84
(2) INFORMATION FOR SEQ ID NO:17:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 81 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:	
GCTGCCACTC TGTTGACAGT AATAGACTGC AAAATCTTCA GGCTCCAGAC TGGAGATAGT	60
GAGGGTGAAA TCTGTCCCTG A	81
(2) INFORMATION FOR SEQ ID NO:18:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 57 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:	
CAACAGAGTG GCAGCTGGCC TCACACGTTC GGAGGGGGGA CCAAGGTGGA AATTAAG	57
(2) INFORMATION FOR SEQ ID NO:19:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 36 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	

36

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GCCCAACCAG CCATGGCCGA TATTGTGCTA ACTCAG

(2	2) INFORMATION FOR SEQ ID NO:20:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:	
AC	CAGTTGGTG CAGCATCAGC	20
(2	2) INFORMATION FOR SEQ ID NO:21:	
٠٠	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 36 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:	
AC	CCCCTGTGG CAAAAGCCGA AGTGCAGCTG GTGGAG	36
(2	2) INFORMATION FOR SEQ ID NO:22:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:	
G <i>I</i>	ATGGGGGTG TCGTTTTGGC	20
(2	2) INFORMATION FOR SEQ ID NO:23:	
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 10 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: peptide	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:	
	Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser 1 5 10	
(2	2) INFORMATION FOR SEQ ID NO:24:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	

(ix) FEATURE:

- (A) NAME/KEY: misc_feature (B) LOCATION: 11..13
- (D) OTHER INFORMATION: /note= ""NNN" represents a codon specifying any amino acid other than Lys."
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GGGAACGATA NNNGATGAGA AGC

23

Bild